Vet.Rec. 1990 Aug 18;127(7):168-9.

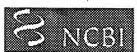
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Detection of antibody to Salmonella enteritidis by a gm flagellin-based ELISA.

Timoney JF, Sikora N, Shivaprasad HL, Opitz M.

Department of Veterinary Microbiology, Immunology and Parasitology, New York State College of Veterinary Medicine, Cornell University, Ithaca 14853.

PMID: 2219649 [PubMed - indexed for MEDLINE]







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□ 16	Mizumoto N. Toyota-Hanatani Y. Sasai K. Tani H. Ekawa T. Ohta H. Baba E.	Related Articles, Links
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	Monoclonal antibody-based detection system for Salm Avian Dis. 1993 Apr-Jun;37(2):501-7. PMID: 8363514 [PubMed - indexed for MEDLINE]	onella enteritidis.
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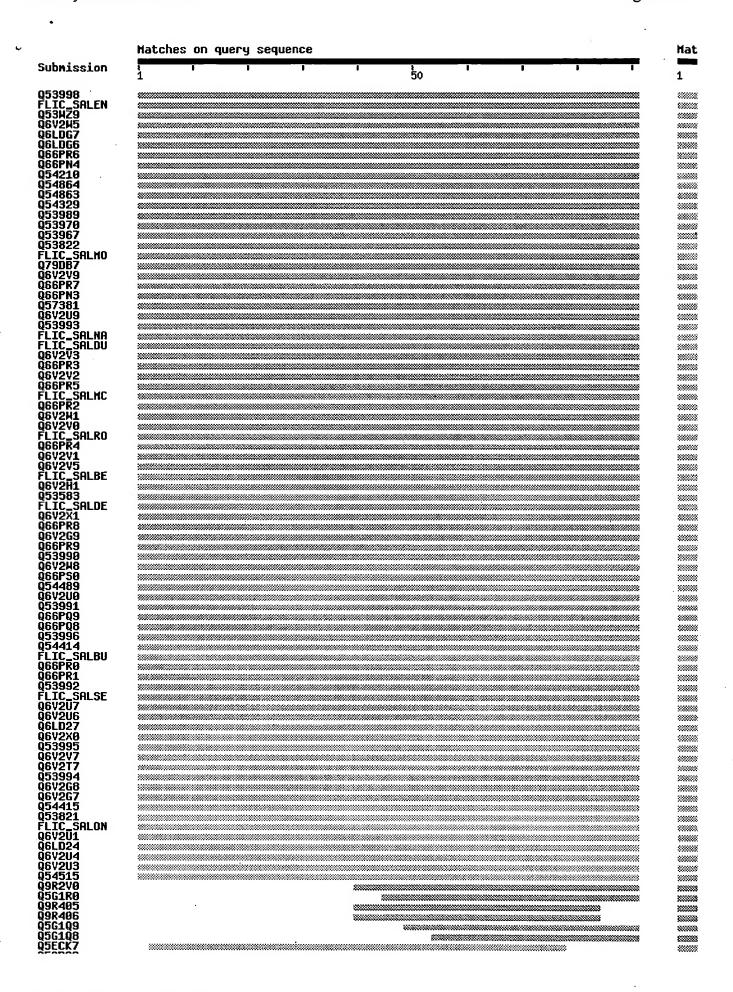
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Alignments

tr Q53998 Phase-1 flagellin (Fragment) [flic] [Salmonella 493 Q53998_SALEN enteritidis] AA align

Score = 181 bits (460), Expect = 2e-45 Identities = 91/91 (100%), Positives = 91/91 (100%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG Sbjct: 245 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 304

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91
ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK
Sbjct: 305 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 335

sp Q06972 Flagellin (Phase-1-C flagellin) [fliC] [Salmonella 504
FLIC_SALEN enteritidis] AA
align

Score = 179 bits (454), Expect = 1e-44Identities = 90/91 (98%), Positives = 90/91 (98%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60
TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG
Sbjct: 256 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 315

Query: 61 ATDVNAATLQSSKNYYTSVVNGQFTFDDKTK 91 ATDVNAATLQSSKNYYTSVVNGQFTFDDKTK Sbjct: 316 ATDVNAATLQSSKNYYTSVVNGQFTFDDKTK 346

tr Q53WZ9 Phase 1 flagellin [fliC] [Salmonella 505 AA Q53WZ9_SALEN enteritidis] align

Score = 179 bits (454), Expect = 1e-44 Identities = 90/91 (98%), Positives = 90/91 (98%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60
TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG
Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91
ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK
Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr Q6V2W5 Phase 1 flagellin [flic] [Salmonella 505 AA Q6V2W5_9ENTR enterica] align

Score = 179 bits (454), Expect = 1e-44Identities = 90/91 (98%), Positives = 90/91 (98%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60
TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91

ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr Q6LDG7 Phase-1 flagellin [fliC1] [Salmonella 505 AA Q6LDG7_SALGL gallinarum] align

Score = 179 bits (454), Expect = 1e-44Identities = 90/91 (98%), Positives = 90/91 (98%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr Q6LDG6 Phase-1 flagellin [fliC1] [Salmonella enterica subsp. 505
Q6LDG6_SALET enterica AA
serovar Gallinarum/pullorum] align

Score = 179 bits (454), Expect = 1e-44 Identities = 90/91 (98%), Positives = 90/91 (98%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGÉKVTLTVADIATG 60 TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr Q66PR6 Phase 1 flagellin [flic] [Salmonella enterica subsp. 505
Q66PR6_SALET enterica serovar Enteritidis] AA

Score = 179 bits (454), Expect = 1e-44 Identities = 90/91 (98%), Positives = 90/91 (98%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60
TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91

ATDVNAATLOSSKNVYTSVVNGOFTFDDKTK

Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr <u>Q66PN4</u> Phase 1 flagellin [fliC] [Salmonella enterica subsp. 505 Q66PN4_SALET enterica AA serovar Emek] aliqn

Score = 179 bits (454), Expect = 1e-44 Identities = 90/91 (98%), Positives = 90/91 (98%)

 ${\tt Query:~1~TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG~60}$

TAEAKAL GAIKGGEEGDTEDYEGVTETIDTETGDDGNGEVSTTINGEEVTLTVADIATG

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91

ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr Q54210 Phase-1 flagellin [fliC1] [Salmonella 494 AA Q54210_SALGL gallinarum] align

Score = 179 bits (454), Expect = 1e-44 Identities = 90/91 (98%), Positives = 90/91 (98%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91

ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr Q54864 Phase-1 flagellin [fliC] [Salmonella 505 AA Q54864_SALPU pullorum] align

Score = 177 bits (450), Expect = 3e-44 Identities = 89/91 (97%), Positives = 90/91 (98%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 WAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91

ATDVNAATLQSSKNVYTSVVNG+FTFDDKTK

Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGKFTFDDKTK 347

tr Q54863 Phase-1 flagellin [fliC] [Salmonella 505 AA Q54863 SALPU pullorum] align Score = 177 bits (450), Expect = 3e-44Identities = 89/91 (97%), Positives = 90/91 (98%) TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 Ouerv: 1 TABAKAI GAIKGGKEGDTFDYKGVTFTTDTKTGDDGNGKVSTTINGEKVTLTVADIATG Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316 Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 ATDVNAATLQSSKNVYTSVVNG+FTFDDKTK -Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGKFTFDDKTK 347 tr Q54329 Phase-1 flagellin (Fragment) [flic] [Salmonella enterica 504 Q54329 SALET subsp. enterica serovar Enteritidis var. jena] aliqn Score = 177 bits (449), Expect = 4e-44Identities = 89/91 (97%), Positives = 90/91 (98%) TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTG+DGNGKVSTTINGEKVTLTVADIATG Sbjct: 256 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGNDGNGKVSTTINGEKVTLTVADIATG 315 Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 ATDVNAATLQSSKNVYTSVVNGQETFDDKTK Sbjct: 316 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 346 tr Q53989 Phase-1 flagellin (Fragment) [flic] [Salmonella enterica 504 Q53989 SALET subsp. AΑ enterica serovar Essen] align Score = 177 bits (449), Expect = 4e-44Identities = 89/91 (97%), Positives = 90/91 (98%) TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 Query: 1 TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTG+DGNGKVSTTINGEKVTLTVADIATG Sbjct: 256 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGNDGNGKVSTTINGEKVTLTVADIATG 315 Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK Sbjct: 316 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 346 tr Q53970 Phase-1 flagellin [fliC1] [Salmonella 505 AA Q53970 SALDU . dublin] align Score = 177 bits (449), Expect = 4e-44Identities = 89/91 (97%), Positives = 89/91 (97%)

TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316 Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 A DVNAATLQSSKNVYTSVVNGQETEDDKTK Sbjct: 317 AADVNAATLQSSKNVYTSVVNGQFTFDDKTK 347 tr Q53967 Phase-1 flagellin (Fragment) [fliC] [Salmonella enterica Q53967 SALET subsp. enterica serovar Enteritidis var. danysz] align Score = 177 bits (449), Expect = 4e-44Identities = 89/91 (97%), Positives = 90/91 (98%) Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTG+DGNGKVSTTINGEKVTLTVADIATG Sbjct: 256 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGNDGNGKVSTTINGEKVTLTVADIATG 315 Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 ATDVNAATLQSSKNVYTSVVNGQETEDDKTK Sbjct: 316 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 346 tr Q53822 Phase-1 flagellin (Fragment) [flic] [Salmonella enterica 504 Q53822 SALET subsp. enterica serovar Enteritidis var. chaco] align Score = 177 bits (449), Expect = 4e-44Identities = 89/91(97%), Positives = 90/91(98%)TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 Query: 1 TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTG+DGNGKVSTTINGEKVTLTVADIATG Sbjct: 256 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGNDGNGKVSTTINGEKVTLTVADIATG 315 Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 ATDVNAATLQSSKNVYTSVVNGQETEDDKTK Sbjct: 316 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 346 504 sp Q06973 Flagellin (Phase-1-C flagellin) [flic] [Salmonella FLIC SALMO montevideo] AA align

Score = 177 bits (448), Expect = 6e-44 Identities = 89/91 (97%), Positives = 89/91 (97%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 T EAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG Sbjct: 256 TDEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 315

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91

ATDVNAATLOSSKNYYTSVVNGOETEDDKTK

Sbjct: 316 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 346

tr Q79DB7 Phase 1 flagellin [flic] [Salmonella enterica subsp. 505 Q79DB7_SALET enterica serovar Othmarschen] AA

Score = 177 bits (448), Expect = 6e-44Identities = 89/91 (97%), Positives = 89/91 (97%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIAT 60
TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIAT

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATS 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91
ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347.

tr Q6V2V9 Phase 1 flagellin [flic] [Salmonella 505 AA Q6V2V9_9ENTR enterica] align

Score = 177 bits (448), Expect = 6e-44 Identities = 89/91 (97%), Positives = 89/91 (97%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 T EAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG

Sbjct: 257 TDEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91
ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr Q66PR7_SALMO Phase 1 flagellin [flic] [Salmonella 505 AA montevideo] align

Score = 177 bits (448), Expect = 6e-44 Identities = 89/91 (97%), Positives = 89/91 (97%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60
T EAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG

Sbjct: 257 TDEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr <u>Q66PN3</u> Phase 1 flagellin [flic] [Salmonella enterica subsp. 505

Q66PN3_SALET enterica serovar Enteritidis]

AA align

Score = 177 bits (448), Expect = 6e-44 Identities = 89/91 (97%), Positives = 89/91 (97%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 T EAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG Sbjct: 257 TDEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91
ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr Q57381 Phase-1 flagellin [fliC1] [Salmonella 505 AA Q57381_SALEN enteritidis] align

Score = 177 bits (448), Expect = 6e-44 Identities = 89/91 (97%), Positives = 89/91 (97%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIAT

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATS 316

Query: 61. ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr Q6V2U9 Phase 1 flagellin [flic] [Salmonella 505 AA Q6V2U9_9ENTR enterica] align

Score = 176 bits (447), Expect = 8e-44 Identities = 89/91 (97%), Positives = 89/91 (97%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60
TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGD GNGKVSTTINGEKVTLTVADIATG
Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDGGNGKVSTTINGEKVTLTVADIATG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91
ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK
Sbjct: 317 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr Q53993 Phase 1 flagellin [flic] [Salmonella 508 AA Q53993_9ENTR enterica] align

Score = 176 bits (446), Expect = 1e-43
Identities = 88/91 (96%), Positives = 89/91 (97%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 TAEAKAI GAIKGGKEGDTFDYKGV+FTIDTKTGDDGNGKVSTTINGEKVTLTVADI TG

Sbjct: 260 TAEAKAIAGAIKGGKEGDTFDYKGVSFTIDTKTGDDGNGKVSTTINGEKVTLTVADITTG 319

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91

ATDVNAATLQSSKNVYTSVVNGQETFDDKTK

Sbjct: 320 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 350

sp 052959 Phase-1 flagellin [flic] [Salmonella 504 AA FLIC_SALNA naestved] align

Score = 175 bits (443), Expect = 2e-43 Identities = 88/91 (96%), Positives = 88/91 (96%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60

TABAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIA G

Sbjct: 256 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIAIG 315

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91

A DVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 316 AADVNAATLQSSKNVYTSVVNGQFTFDDKTK 346

sp Q06971 Flagellin (Phase-1-C flagellin) [fliC] [Salmonella dublin] 504 AA FLIC_SALDU

align

Score = 175 bits (443), Expect = 2e-43 Identities = 88/91 (96%), Positives = 88/91 (96%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60

TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIA G

Sbjct: 256 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIAIG ,315

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91

A DYNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 316 AADVNAATLQSSKNVYTSVVNGQFTFDDKTK 346

tr Q6V2V3 Phase 1 flagellin [fliC] [Salmonella 505 AA Q6V2V3_9ENTR enterica] align

Score = 175 bits (443), Expect = 2e-43

Identities = 88/91 (96%), Positives = 88/91 (96%)

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60

TAEAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGMGKVSTTINGEKVTITVADIA G

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIAIG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91

A DVNAATLQSSKNVYTSVVNGQETFDDKTK

Sbjct: 317 AADVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

Q66PR3 tr Phase 1 flagellin [fliC] [Salmonella 5:05 AA Q66PR3 SALDU dublin] align

Score = 175 bits (443), Expect = 2e-43Identities = 88/91 (96%), Positives = 88/91 (96%)

TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 TABAKAI GAIKGGKEGDTEDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIA G

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIAIG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 A DVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 317 AADVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

tr Q6V2V2 Phase 1 flagellin [fliC] [Salmonella 505 AA Q6V2V2 9ENTR enterica] align

Score = 175 bits (443), Expect = 2e-43Identities = 88/91 (96%), Positives = 88/91 (96%)

TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60

TAKAKAI GAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIA G

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIAIG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91 A DVNAATLQSSKNVYTSVVNGQFTFDDKTK

Sbjct: 317 AADVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

505 AA trQ66PR5 Phase 1 flagellin [fliC] [Salmonella Q66PR5 SALNA

Score = 175 bits (443), Expect = 2e-43Identities = 88/91 (96%), Positives = 88/91 (96%)

naestved]

Query: 1 TAEAKAIRGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIATG 60 TABAKAI GAIKGGKEGDTFDYKGVTFTTDTKTGDDGNGKVSTTINGEKVTLTVADIA G

Sbjct: 257 TAEAKAIAGAIKGGKEGDTFDYKGVTFTIDTKTGDDGNGKVSTTINGEKVTLTVADIAIG 316

Query: 61 ATDVNAATLQSSKNVYTSVVNGQFTFDDKTK 91

A DVNAATLQSSKNVYTSVVNGQETFDDKTK

Sbjct: 317 AADVNAATLQSSKNVYTSVVNGQFTFDDKTK 347

align

WEST Search History

Hide Items Restore Clear Cancel

DATE: Thursday, July 07, 2005

Hide?	<u>Set</u> Name	Query	<u>Hit</u> Count	
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND				
	L1	(flic or fli-c or ((phase near2 1) or (phase-1-c or phase1c or phase1-c)) near5 flagell\$2)	15316	
	L2	L1 and enteritidis	10	
	L3	flic.clm.	8	
	L4	L3 not 12	7	
	L5	(enteritidis or enteriditis).clm.	135	
	L6	pili or pillin or pilin or fimbria or fimbriae or fimbrial or fimbrial or fimbrin	23100	
	L7	fime or sef14 or sef-14 ro sef21 or sef-21 or sef17 or sef-17	250	
	L8 .	L7 or 16	23241	
	L9	(sef14 or sef-14 ro sef21 or sef-21 or sef17 or sef-17).clm.	1	
	L10	(fla or flagella or flagellin).clm.	119	
	L11	11.clm.	8	
	L12	L11 not 13	0	
	L13	Ll5 and l10 not 19	. 0	

END OF SEARCH HISTORY

WEST Search History

Hide Items Restore Clear Cancel

DATE: Thursday, July 07, 2005

Hide?	<u>Set</u> Name	Query	<u>Hit</u> Count	
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND				
	L1	(flic or fli-c or ((phase near2 1) or (phase-1-c or phase1c or phase1-c)) near5 flagell\$2)	15316	
	L2	L1 and enteritidis	10	
	L3	flic.clm.	8	
	L4	L3 not 12	7	
	L5	(enteritidis or enteriditis).clm.	135	
	L6	pili or pillin or pilin or fimbria or fimbriae or fimbrial or fimbrial or fimbrin	23100	
	L7	fime or sef14 or sef-14 ro sef21 or sef-21 or sef17 or sef-17	250	
	L8	L7 or 16	23241	
	L9	(sef14 or sef-14 ro sef21 or sef-21 or sef17 or sef-17).clm.	1	
	L10	(fla or flagella or flagellin).clm.	119	
	L11	11.clm.	8	
. 🗀	L12	L11 not 13	0	
	L13	L15 and 110 not 19	0	

END OF SEARCH HISTORY